

## SEQUENCE LISTING

<110> KIM, Jin-Woo

<120> HUMAN CERVICAL CANCER 1 PROTOONCOGENE AND PROTEIN ENCODED THEREIN

<130> KIM

<150> KR 1999-44811

<151> 1999-10-15

<150> PCT/KR00/00284

<151> 2000-03-30

<160> 7

<170> PatentIn version 3.0

<210> 1

<211> 2118

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (9)..(1088)

<220>

<221> sig\_peptide

<222> (9)..(83)

<220>

<221> misc\_feature

<222> (435)..(494)

<223> transmembrane domain

<400> 1

ctgtgaag	atg gcg ctc tcc agg gtg tgc tgg gct cgg tcg gct gtg tgg	50
	Met Ala Leu Ser Arg Val Cys Trp Ala Arg Ser Ala Val Trp	
1	5	10

  

ggc tcg gca gtc acc cct gga cat ttt gtc acc cgg agg ctg caa ctt	98
Gly Ser Ala Val Thr Pro Gly His Phe Val Thr Arg Arg Leu Gln Leu	
15	20

  

ggt cgc tct ggc ctg gct tgg ggg gcc cct cgg tct tca aag ctt cac	146
Gly Arg Ser Gly Leu Ala Trp Gly Ala Pro Arg Ser Ser Lys Leu His	
35	40



ctt tct cca aag gca gat gtg aag aac ttg atg tct tat gtg gta acc 194  
 Leu Ser Pro Lys Ala Asp Val Lys Asn Leu Met Ser Tyr Val Val Thr  
 50 55 60

aag aca aaa gcg att aat ggg aaa tac cat cgt ttc ttg ggt cgt cat 242  
 Lys Thr Lys Ala Ile Asn Gly Lys Tyr His Arg Phe Leu Gly Arg His  
 65 70 75

ttc ccc cgc ttc tat atc ctg tac aca atc ttc atg aaa gga ttg cag 290  
 Phe Pro Arg Phe Tyr Ile Leu Tyr Thr Ile Phe Met Lys Gly Leu Gln  
 80 85 90

atg tta tgg gct gat gcc aaa aag gct aga aga ata aag aca aat atg 338  
 Met Leu Trp Ala Asp Ala Lys Lys Ala Arg Arg Ile Lys Thr Asn Met  
 95 100 105 110

tgg aag cac aat ata aag ttt cat caa ctt cca tac cgg gag atg gag 386  
 Trp Lys His Asn Ile Lys Phe His Gln Leu Pro Tyr Arg Glu Met Glu  
 115 120 125

cat ttg aga cag ttc cgc caa gac gtc acc aag tgt ctt ttc cta ggt 434  
 His Leu Arg Gln Phe Arg Gln Asp Val Thr Lys Cys Leu Phe Leu Gly  
 130 135 140

att att tcc att cca cct ttt gcc aac tac ctg gtc ttc ttg cta atg 482  
 Ile Ile Ser Ile Pro Pro Phe Ala Asn Tyr Leu Val Phe Leu Leu Met  
 145 150 155

tac ctg ttt ccc agg caa cta ctg atc agg cat ttc tgg acc cca aaa 530  
 Tyr Leu Phe Pro Arg Gln Leu Leu Ile Arg His Phe Trp Thr Pro Lys  
 160 165 170

caa caa act gat ttc tta gat atc tat cat gct ttc cgg aag cag tcc 578  
 Gln Gln Thr Asp Phe Leu Asp Ile Tyr His Ala Phe Arg Lys Gln Ser  
 175 180 185 190

cac cca gaa att att agt tat tta gaa aag gtc atc cct ctc att tct 626  
 His Pro Glu Ile Ile Ser Tyr Leu Glu Lys Val Ile Pro Leu Ile Ser  
 195 200 205

gat gca gga ctc cgg tgg cgt ctg aca gat ctg tgc acc aag ata cag 674  
 Asp Ala Gly Leu Arg Trp Arg Leu Thr Asp Leu Cys Thr Lys Ile Gln  
 210 215 220

cgt ggt acc cac cca gca ata cat gat atc ttg gct ctg aga gag tgt 722  
 Arg Gly Thr His Pro Ala Ile His Asp Ile Leu Ala Leu Arg Glu Cys  
 225 230 235



ttc tct aac cat cct ctg ggc atg aac caa ctc cag gct ttg cac gtg 770  
 Phe Ser Asn His Pro Leu Gly Met Asn Gln Leu Gln Ala Leu His Val  
 240 245 250

aaa gcc ttg agc cgg gcc atg ctt ctc aca tct tac ctg cct cct ccc 818  
 Lys Ala Leu Ser Arg Ala Met Leu Leu Thr Ser Tyr Leu Pro Pro Pro  
 255 260 265 270

ttg ttg aga cat cgt ttg aag act cat aca act gtg att cac caa ctg 866  
 Leu Leu Arg His Arg Leu Lys Thr His Thr Thr Val Ile His Gln Leu  
 275 280 285

gac aag gct ttg gca aag ctg ggg att ggc cag ctg act gct cag gaa 914  
 Asp Lys Ala Leu Ala Lys Leu Gly Ile Gly Gln Leu Thr Ala Gln Glu  
 290 295 300

gta aaa tcg gct tgt tat ctc cgt ggc ctg aat tct acg cat att ggt 962  
 Val Lys Ser Ala Cys Tyr Leu Arg Gly Leu Asn Ser Thr His Ile Gly  
 305 310 315

gaa gat agg tgt cga act tgg ctg gga gaa tgg ctg cag att tcc tgc 1010  
 Glu Asp Arg Cys Arg Thr Trp Leu Gly Glu Trp Leu Gln Ile Ser Cys  
 320 325 330

agc ctg aaa gaa gct gag ctg tct ctc ttg ctg cac aac gtg gtc ctg 1058  
 Ser Leu Lys Glu Ala Glu Leu Ser Leu Leu Leu His Asn Val Val Leu  
 335 340 345 350

ctc tcc acc aac tac ctt ggg aca agg cgc tgaatgaacc atggagcggg 1108  
 Leu Ser Thr Asn Tyr Leu Gly Thr Arg Arg  
 355 360

tggcattgtc ctgcagtcgt atagtatagc agtgcaggaa caaacagcac ttgccagcaa 1168

agtctgtgtg tactgttaag tgtgtgggag gcagagagag gagcaggggc catgggcttc 1228

acagcatggc acacctgtgg gaactgcaga cattcctctc acagctagaa ctgaaacaaa 1288

cctctttgct aggggtggtc cgtgtgaggt gtcacctgt cccctcata attactaata 1348

gctggaactg gcagcagcct ctactgggct ttactgtga tgtgttcagt tcatgtccta 1408

ggaagtcagc ttttgcccca ggtgggaatc cttatttggc ttaggactga tccacttcca 1468

tgttacttac atctgtgggt tttgttgtt gctgttagaa aatttttggc tggtgaaaac 1528

agcactcctt tggctggagc acttgtgtcc atgcatgtac ttgggtgttt cctccatcc 1588

tttctgatat gacaaaaat caagttgttt tgttttttgt caccttcaact ggcatgggct 1648



```

aaccacttct ttttcaaacc ctctgaacac ctttttctga tgggtaactt gcaggaatat 1708
tctattggaa aagataacag gaagtacaag tgcttcttga ccccttctc aatgtttcta 1768
gccttcactc tccattgtct tttctgggct gtattacagc cctctgtgga tcttcaactc 1828
tgctgcctcc actgtgatgc agcagtccaa ctgtaactga cagtggctgc cttctctggg 1888
ccatggatca cacctgtaag gtactaatta ctgcccagcc tggggagatc aggagaggtc 1948
tgcatagtta gtaagttggg tttagctttt gtgtgtgcat cagtgactta gagttctgta 2008
ataacttatt gtaaattgat gaagcactgt ttttaaacc aagtaaagac tgcttgaaac 2068
ctgttgatgg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2118

```

```

<210> 2
<211> 360
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (435)..(494)
<223> transmembrane domain

<400> 2

```

```

Met Ala Leu Ser Arg Val Cys Trp Ala Arg Ser Ala Val Trp Gly Ser
1           5           10           15

```

```

Ala Val Thr Pro Gly His Phe Val Thr Arg Arg Leu Gln Leu Gly Arg
20           25           30

```

```

Ser Gly Leu Ala Trp Gly Ala Pro Arg Ser Ser Lys Leu His Leu Ser
35           40           45

```

```

Pro Lys Ala Asp Val Lys Asn Leu Met Ser Tyr Val Val Thr Lys Thr
50           55           60

```

```

Lys Ala Ile Asn Gly Lys Tyr His Arg Phe Leu Gly Arg His Phe Pro
65           70           75           80

```



Arg Phe Tyr Ile Leu Tyr Thr Ile Phe Met Lys Gly Leu Gln Met Leu  
85 90 95

Trp Ala Asp Ala Lys Lys Ala Arg Arg Ile Lys Thr Asn Met Trp Lys  
100 105 110

His Asn Ile Lys Phe His Gln Leu Pro Tyr Arg Glu Met Glu His Leu  
115 120 125

Arg Gln Phe Arg Gln Asp Val Thr Lys Cys Leu Phe Leu Gly Ile Ile  
130 135 140

Ser Ile Pro Pro Phe Ala Asn Tyr Leu Val Phe Leu Leu Met Tyr Leu  
145 150 155 160

Phe Pro Arg Gln Leu Leu Ile Arg His Phe Trp Thr Pro Lys Gln Gln  
165 170 175

Thr Asp Phe Leu Asp Ile Tyr His Ala Phe Arg Lys Gln Ser His Pro  
180 185 190

Glu Ile Ile Ser Tyr Leu Glu Lys Val Ile Pro Leu Ile Ser Asp Ala  
195 200 205

Gly Leu Arg Trp Arg Leu Thr Asp Leu Cys Thr Lys Ile Gln Arg Gly  
210 215 220

Thr His Pro Ala Ile His Asp Ile Leu Ala Leu Arg Glu Cys Phe Ser  
225 230 235 240

Asn His Pro Leu Gly Met Asn Gln Leu Gln Ala Leu His Val Lys Ala  
245 250 255

Leu Ser Arg Ala Met Leu Leu Thr Ser Tyr Leu Pro Pro Pro Leu Leu  
260 265 270



Arg His Arg Leu Lys Thr His Thr Thr Val Ile His Gln Leu Asp Lys  
 275 280 285

Ala Leu Ala Lys Leu Gly Ile Gly Gln Leu Thr Ala Gln Glu Val Lys  
 290 295 300

Ser Ala Cys Tyr Leu Arg Gly Leu Asn Ser Thr His Ile Gly Glu Asp  
 305 310 315 320

Arg Cys Arg Thr Trp Leu Gly Glu Trp Leu Gln Ile Ser Cys Ser Leu  
 325 330 335

Lys Glu Ala Glu Leu Ser Leu Leu Leu His Asn Val Val Leu Leu Ser  
 340 345 350

Thr Asn Tyr Leu Gly Thr Arg Arg  
 355 360

<210> 3  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <223> anti-sense DNA

<400> 3  
 cctggacatt ttgtcacc

18

<210> 4  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <223> sense DNA

<400> 4  
 ggtgacaaaa tgtccagg

18

<210> 5



18

20

20